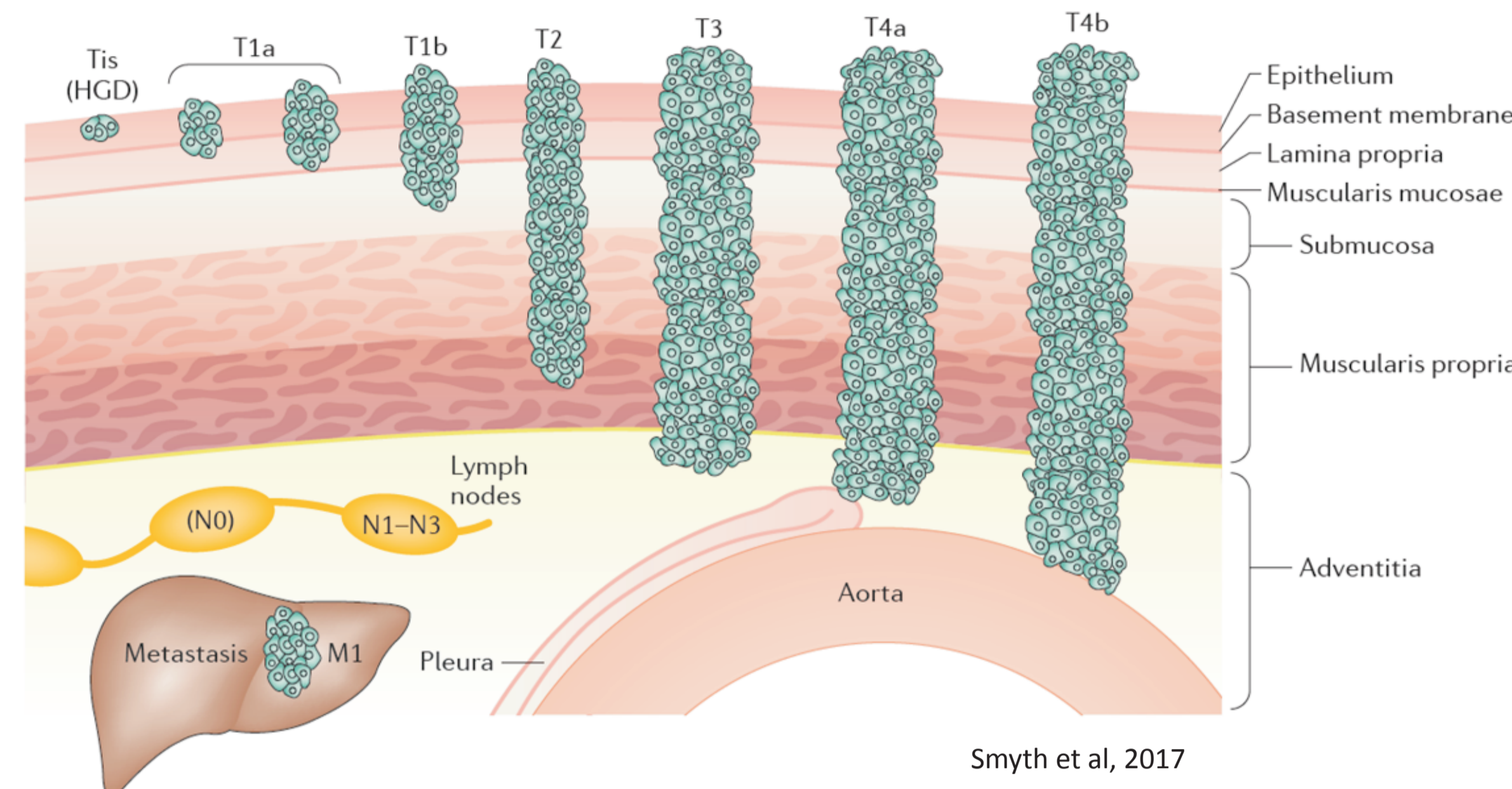


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INTRODUCTION

- Esophageal cancer is the 8th most frequent cancer type and 6th most lethal worldwide (Ferlay et al, 2015)
- The 5-year survival is detected in less than 10% of patients (Cohen and Ajani, 2011)
- Well-established targeted therapies seem to do not benefit ESCC patients, e.g., HER family and downstream proteins (Gonzaga et al, 2012)
- Immune therapy has been used with good results in many different solid tumor, such as melanoma (Robert et al, 2015)



OBJECTIVE

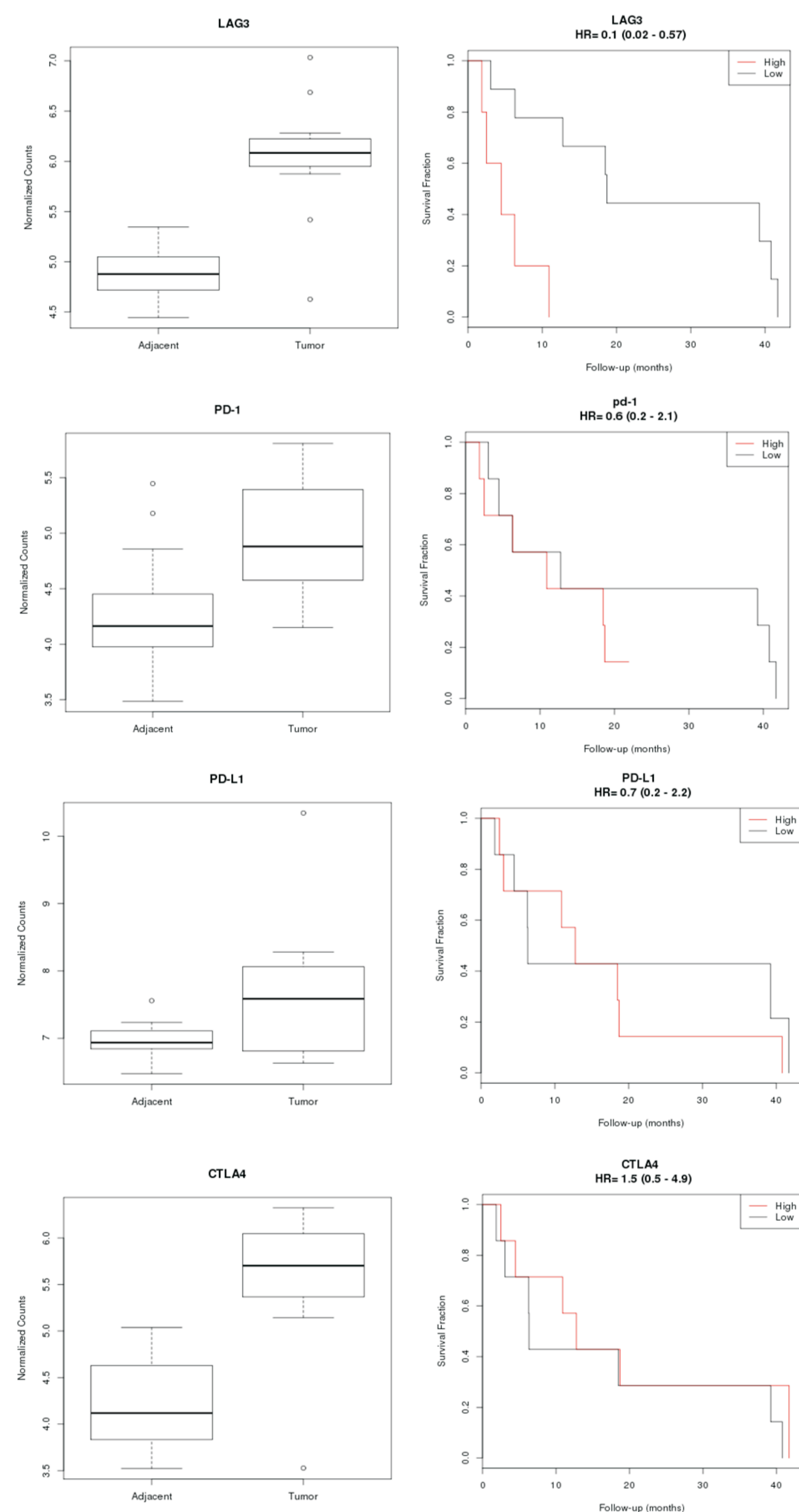
To characterize the immune cells comprising ESCC tumor microenvironment

METHODOLOGY

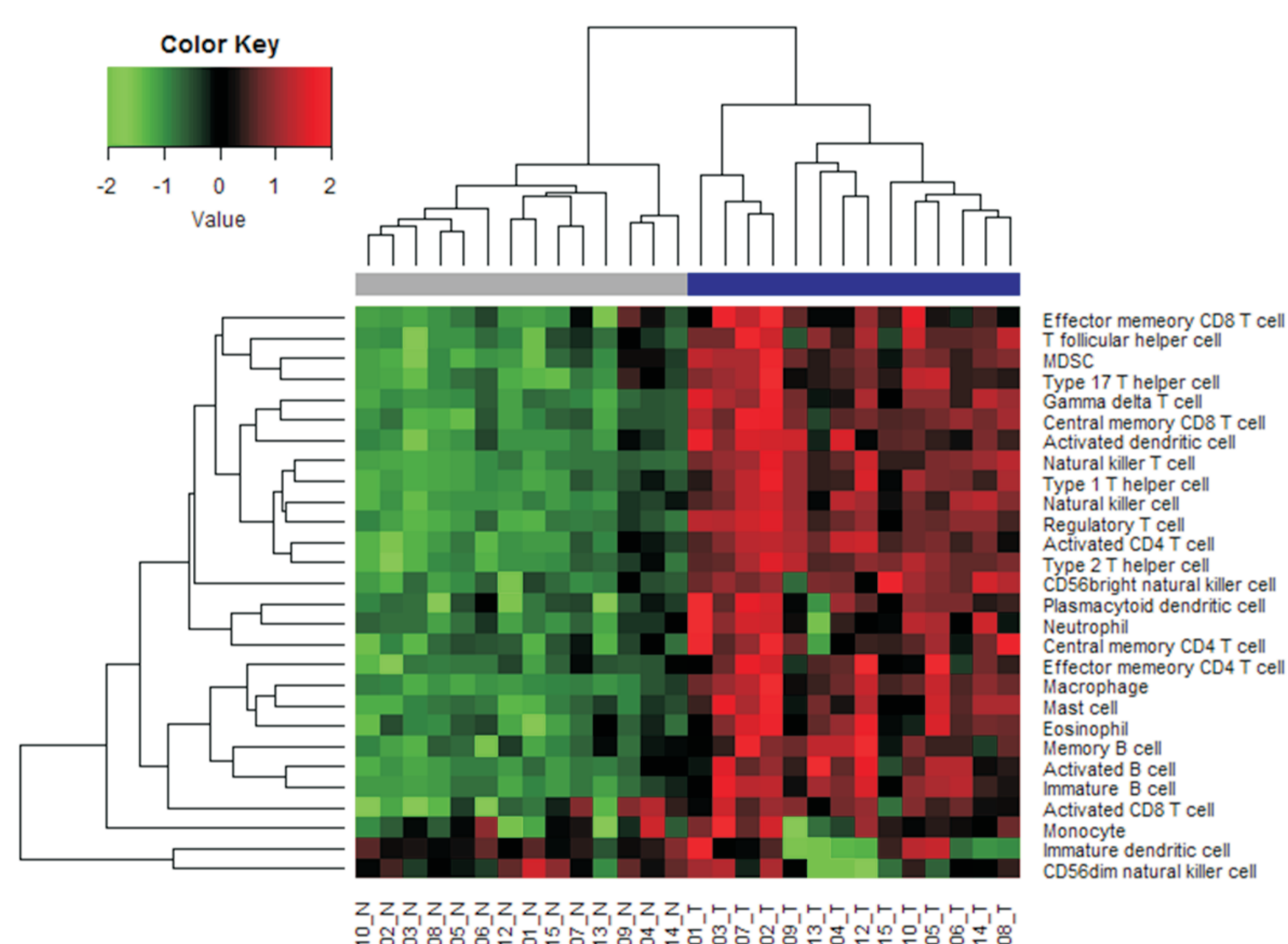
- cDNA libraries of 14 tumor/surrounding mucosa pairs were sequenced in HiSeq2500 sequencer
- To determine the abundance of each immune cell population we applied signatures based on gene expression profile validated by Charoentong et al (2016)
- To identify and quantify BCR rearrangements the MiXCR software was used (Bolotin et al, 2015)
- All further statistical analysis was performed in R

RESULTS

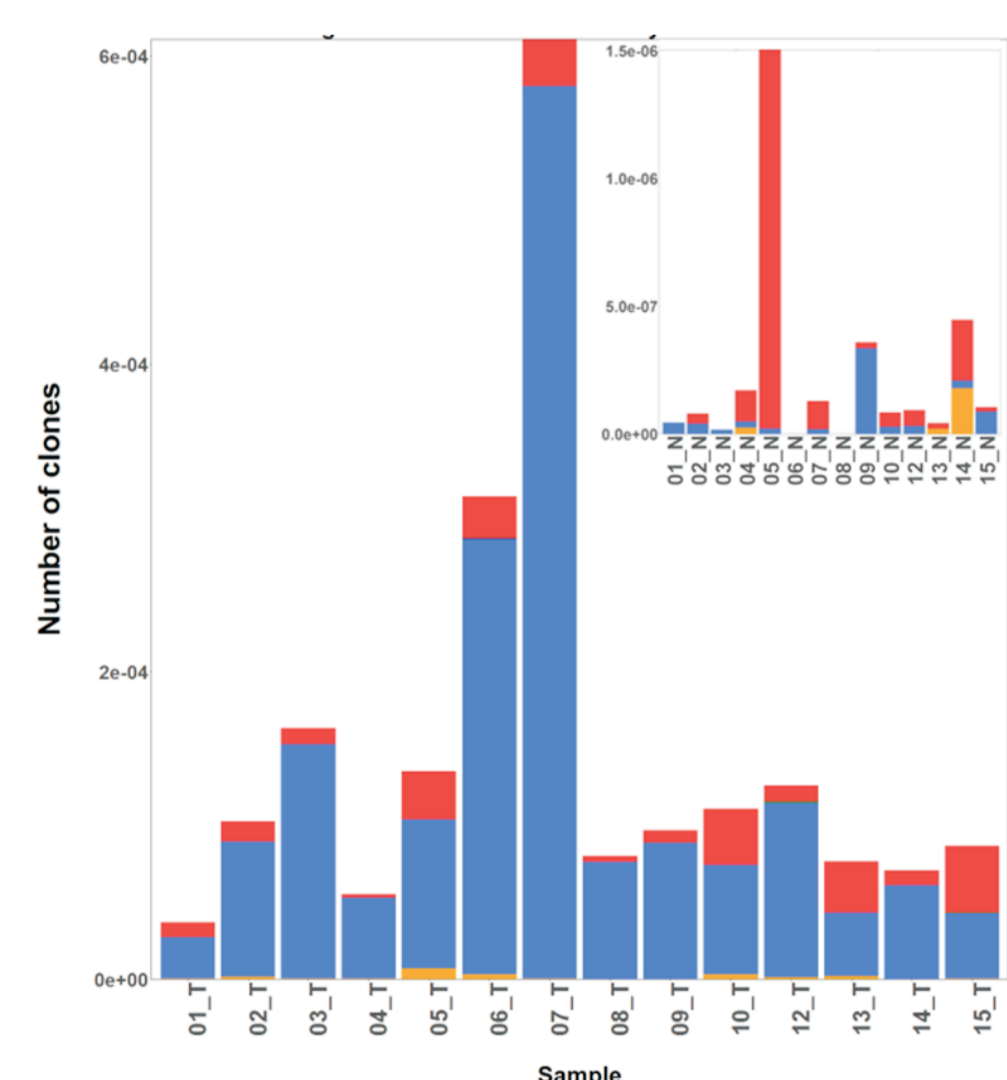
Expression pattern and prognostic impact of the checkpoint immune molecules in ESCC



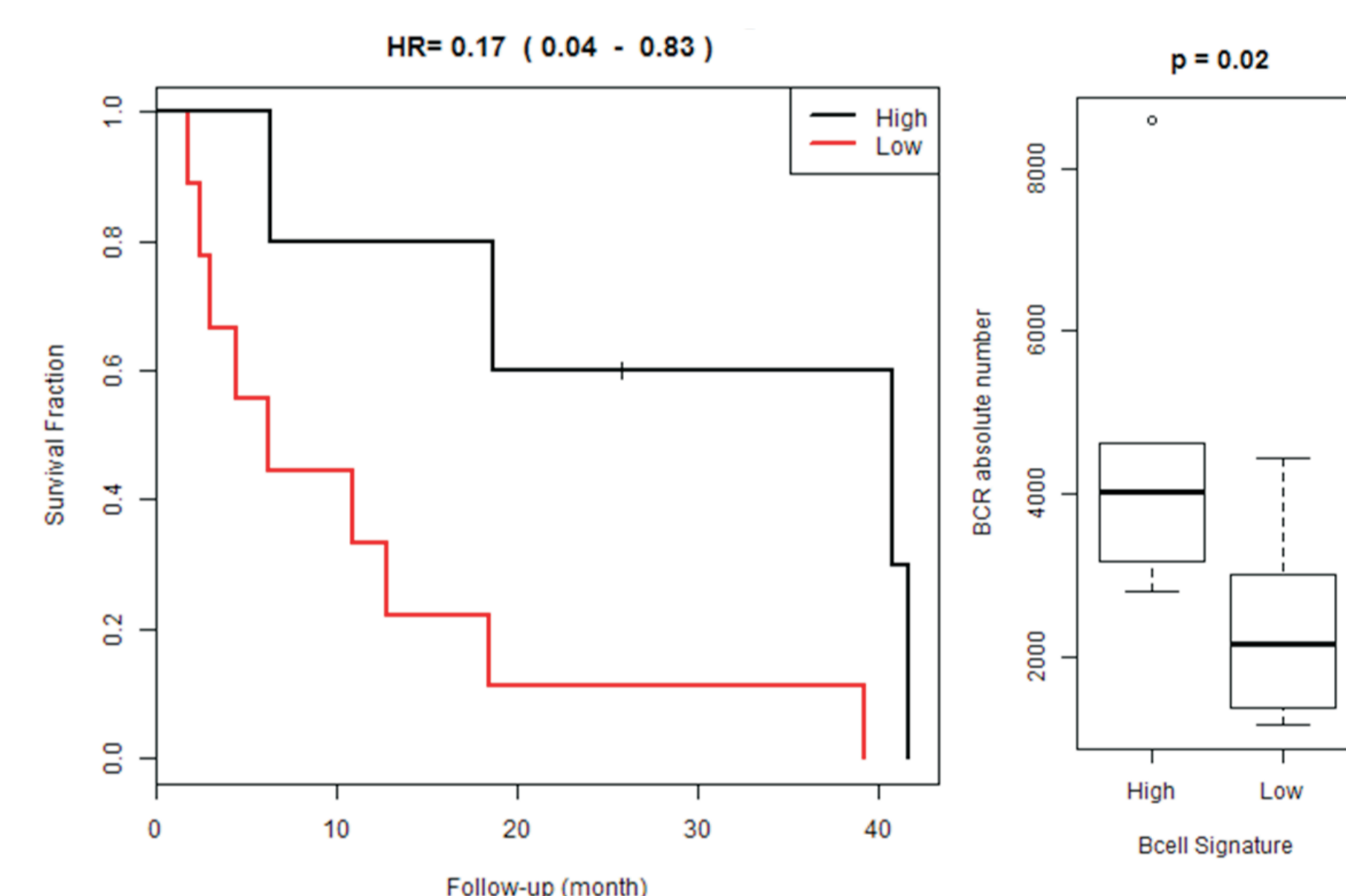
Heatmap with Charoentong immune signatures



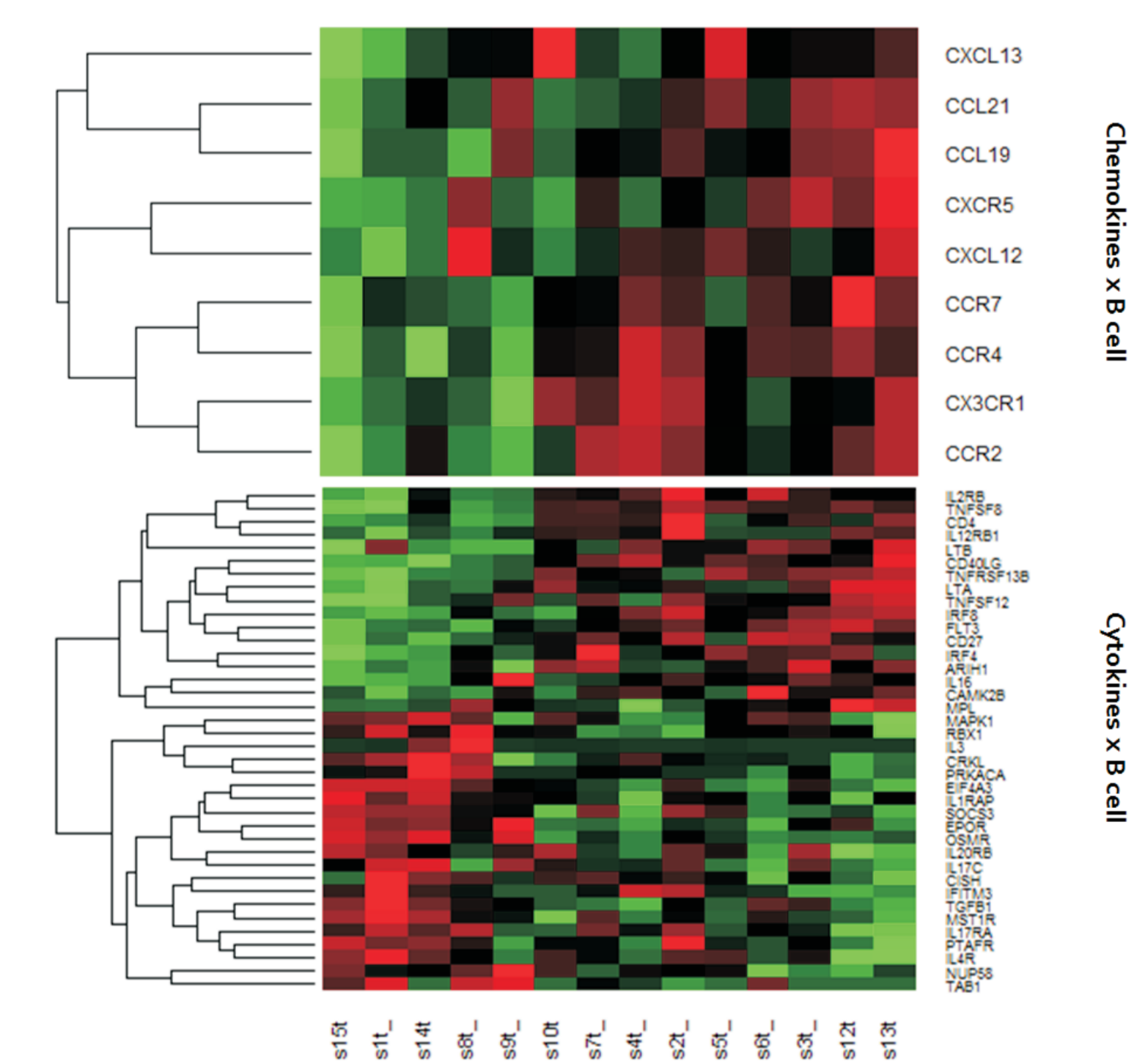
ESCC Immunoglobulin classes normalized by the number of reads



Overall survival – Activated B cell signature and BCR amounts between two signature categories



Differential chemokines and cytokines expression between Activated B cell signature groups



CONCLUSION

B cells may represent an important feature in ESCC tumors and their presence could be associated with an improvement in patients' overall survival

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